

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 09/441,966B

Source: 1FW16

Date Processed by STIC: 11/23/04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 11/23/2004

PATENT APPLICATION: US/09/441,966B

TIME: 14:45:41

Input Set : A:\AERO1120-1.txt

Output Set: N:\CRF4\11222004\I441966B.raw

3 <110> APPLICANT: AEROVANCE, INC.
 4 Hall, Roderick L.
 5 Poll, Christopher T.
 6 Newton, Benjamin B.
 7 Taylor, William J.A.
 9 <120> TITLE OF INVENTION: Method For Accelerating The Rate Of Mucociliary Clearance
 11 <130> FILE REFERENCE: AERO1120-1
 13 <140> CURRENT APPLICATION NUMBER: US 09/441,966B
 14 <141> CURRENT FILING DATE: 1999-11-17
 16 <150> PRIOR APPLICATION NUMBER: US 09/218,913
 17 <151> PRIOR FILING DATE: 1998-12-22
 19 <160> NUMBER OF SEQ ID NOS: 106
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 179
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 30 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
 31 1 5 10 15
 34 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
 35 20 25 30
 38 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
 39 35 40 45
 42 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
 43 50 55 60
 46 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
 47 65 70 75 80
 50 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser
 51 85 90 95
 54 Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr
 55 100 105 110
 58 Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg
 59 115 120 125
 62 Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn
 63 130 135 140
 66 Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln
 67 145 150 155 160
 70 Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly
 71 165 170 175
 74 Ala Val Ser
 78 <210> SEQ ID NO: 2
 79 <211> LENGTH: 197

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80 <212> TYPE: PRT

81 <213> ORGANISM: Homo sapiens

83 <220> FEATURE:

84 <221> NAME/KEY: SIGNAL

85 <222> LOCATION: (1) .. (18)

86 <223> OTHER INFORMATION:

W--> 89 <400> 2

91 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val

92 1 5 10 15

95 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser

96 20 25 30

99 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn

100 35 40 45

103 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly

104 50 55 60

107 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala

108 65 70 75 80

111 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala

112 85 90 95

115 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp

116 100 105 110

119 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala

120 115 120 125

123 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val

124 130 135 140

127 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn

128 145 150 155 160

131 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg

132 165 170 175

135 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu

136 180 185 190

139 Ala Gly Ala Val Ser

140 195

143 <210> SEQ ID NO: 3

144 <211> LENGTH: 153

145 <212> TYPE: PRT

146 <213> ORGANISM: Homo sapiens

148 <400> SEQUENCE: 3

150 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala

151 1 5 10 15

154 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu

155 20 25 30

158 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys

159 35 40 45

162 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn Ala Thr Gly

163 50 55 60

166 Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val Pro Ser Ala

167 65 70 75 80

170 Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met Phe Asn Tyr

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```

171          85          90          95
174 Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser
175          100          105          110
178 Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe
179          115          120          125
182 Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu
183          130          135          140
186 Ala Cys Met Leu Arg Cys Phe Arg Gln
187 145          150
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 58
192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 4
197 Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala
198 1          5          10          15
201 Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu
202          20          25          30
205 Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys
206          35          40          45
209 Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
210          50          55
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 51
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 5
220 Cys Leu Val Ser Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg
221 1          5          10          15
224 Trp Trp Tyr Asn Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly
225          20          25          30
228 Gly Cys Asp Gly Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu
229          35          40          45
232 Lys Lys Cys
233          50
236 <210> SEQ ID NO: 6
237 <211> LENGTH: 58
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 6
243 Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala
244 1          5          10          15
247 Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn
248          20          25          30
251 Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu
252          35          40          45
255 Glu Ala Cys Met Leu Arg Cys Phe Arg Gln
256          50          55
259 <210> SEQ ID NO: 7

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260 <211> LENGTH: 51
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 7
266 Cys Thr Ala Asn Ala Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg
267 1 5 10 15
270 Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly
271 20 25 30
274 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
275 35 40 45
278 Leu Arg Cys
279 50
282 <210> SEQ ID NO: 8
283 <211> LENGTH: 92
284 <212> TYPE: PRT
285 <213> ORGANISM: Homo sapiens
287 <400> SEQUENCE: 8
289 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
290 1 5 10 15
293 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
294 20 25 30
297 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
298 35 40 45
301 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
302 50 55 60
305 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
306 65 70 75 80
309 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
310 85 90
313 <210> SEQ ID NO: 9
314 <211> LENGTH: 708
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Consensus DNA sequence of human Bikunin (Fig. 3).
321 <220> FEATURE:
322 <221> NAME/KEY: misc_feature
323 <222> LOCATION: (622)..(622)
324 <223> OTHER INFORMATION: "n" is any nucleotide.
327 <220> FEATURE:
328 <221> NAME/KEY: misc_feature
329 <222> LOCATION: (679)..(679)
330 <223> OTHER INFORMATION: "n" is any nucleotide.
333 <220> FEATURE:
334 <221> NAME/KEY: misc_feature
335 <222> LOCATION: (707)..(707)
336 <223> OTHER INFORMATION: "n" is any nucleotide.
339 <400> SEQUENCE: 9
340 ggccggggtcg ttctcgcct ggctgggata gctgctctc tctgggggtcc tggcgccga 60

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```

342 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc 120
344 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg 180
346 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc 240
348 cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc 300
350 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta 360
352 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcaccc tcccacgctg 420
354 gtactttgac gtggagagga actcctgcaa taacttcac tatggaggct gccggggcaa 480
356 taagaacagc tacgctctcg aggaggcctg catgctccgc tgcttccgcc agcaggagaa 540
358 tcctcccctg ccccttggtc caaagtggtt ggttctggcc ggggctgttt cgtgatggtg 600
W--> 360 ttgatccttt tcctggggag cntccatggt cttactgatt ccgggtggca aggaggaacc 660
362 aggagcgtgc cctgcccanc gtctggagct tcggagatga caagggnt 708
365 <210> SEQ ID NO: 10
366 <211> LENGTH: 197
367 <212> TYPE: PRT
368 <213> ORGANISM: Artificial Sequence
370 <220> FEATURE:
371 <223> OTHER INFORMATION: Amino acids -18 to 179 of the translation of the consensus
DNA
372 sequence in Fig. 3.
374 <400> SEQUENCE: 10
376 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
377 1 5 10 15
380 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
381 20 25 30
384 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
385 35 40 45
388 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
389 50 55 60
392 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
393 65 70 75 80
396 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
397 85 90 95
400 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
401 100 105 110
404 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
405 115 120 125
408 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
409 130 135 140
412 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
413 145 150 155 160
416 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
417 165 170 175
420 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
421 180 185 190
424 Ala Gly Ala Val Ser
425 195
428 <210> SEQ ID NO: 11
429 <211> LENGTH: 179
430 <212> TYPE: PRT
431 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/441,966BDATE: 11/23/2004
TIME: 14:45:42Input Set : A:\AERO1120-1.txt
Output Set: N:\CRF4\11222004\I441966B.rawPlease Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 622,679,707
Seq#:11; Xaa Pos. 8,17,19,21,22,23,24,25,26,40,42,45,46,47,52,64,103,112
Seq#:11; Xaa Pos. 114,116,117,118,119,120,121,135,137,140,141,142,147,159
Seq#:12; N Pos. 361,367,384,390
Seq#:14; N Pos. 424,481,509
Seq#:16; N Pos. 3,11,12,17,48,425
Seq#:17; N Pos. 6,401,407
Seq#:48; N Pos. 1358
Seq#:51; N Pos. 46,117,313
Seq#:72; Xaa Pos. 9,11,17,19
Seq#:74; Xaa Pos. 25
Seq#:75; N Pos. 425,482,510
Seq#:76; Xaa Pos. 25
Seq#:77; N Pos. 45,49,118,231,305
Seq#:78; N Pos. 117,123,321
Seq#:79; N Pos. 9,11,222,231,262,267,274
Seq#:80; N Pos. 44,46,76,114,187,268,309,317,332,370
Seq#:81; N Pos. 35,148,235,261,272,293,300,313,320
Seq#:82; N Pos. 56,137,145,159,233
Seq#:83; N Pos. 20,26,95,292,313,314,315
Seq#:84; N Pos. 27,139,223,232,302,310,322,328,357,375,392,398,405,427,437
Seq#:84; N Pos. 449,458,474
Seq#:85; N Pos. 361,367,384,390
Seq#:86; N Pos. 3,11,12,17,48,425
Seq#:87; N Pos. 7,403,409
Seq#:88; N Pos. 48,62,211,232,245,309,318
Seq#:89; N Pos. 424,481,509
Seq#:90; N Pos. 257
Seq#:91; N Pos. 19,147
Seq#:92; N Pos. 33,55,213,228,259,267,324,333,344,387
Seq#:93; N Pos. 306,328,342,365,370,377,382,402
Seq#:94; N Pos. 1,142,339,347
Seq#:95; N Pos. 334,368,376
Seq#:96; N Pos. 108,261
Seq#:97; N Pos. 20,30
Seq#:98; N Pos. 45,102,105,159,174,213,337
Seq#:100; N Pos. 304,309
Seq#:101; N Pos. 24
Seq#:102; N Pos. 61,74,122,184
Seq#:103; N Pos. 7
Seq#:104; N Pos. 32,67,136
Seq#:105; N Pos. 13,19,107

VERIFICATION SUMMARY

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Input Set : A:\AERO1120-1.txt

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L:89 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:86
L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:600
M:341 Repeated in SeqNo=9
L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
M:341 Repeated in SeqNo=11
L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:360
L:704 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:701
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:420
M:341 Repeated in SeqNo=14
L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1410 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:45,Line#:1407
L:1522 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:47,Line#:1519
L:1640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:1320
L:1660 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:49,Line#:1657
L:1800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
M:341 Repeated in SeqNo=51
L:2318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72 after pos.:0
M:341 Repeated in SeqNo=72
L:2378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:16
L:2423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:420
M:341 Repeated in SeqNo=75
L:2449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76 after pos.:16
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0
M:341 Repeated in SeqNo=77
L:2528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:78 after pos.:60
M:341 Repeated in SeqNo=78
L:2587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79 after pos.:0
M:341 Repeated in SeqNo=79
L:2664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80 after pos.:0
M:341 Repeated in SeqNo=80
L:2741 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:81 after pos.:0
M:341 Repeated in SeqNo=81
L:2790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:2837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83
L:2966 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:3025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:360
L:3064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
M:341 Repeated in SeqNo=86
L:3105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:87 after pos.:0
M:341 Repeated in SeqNo=87
L:3170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88 after pos.:0
M:341 Repeated in SeqNo=88

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Input Set : A:\AERO1120-1.txt

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L:3221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89 after pos.:420

M:341 Repeated in SeqNo=89

L:3246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90 after pos.:240

L:3267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0

M:341 Repeated in SeqNo=91

L:3350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:92 after pos.:0

M:341 Repeated in SeqNo=92